



SEQUENCE LISTING

<110> Piddington, Christopher S.
 Petrie, Charles
 Shoemaker, Kimberly E.
 Bishop, Paul D.

<120> ZACE2: A HUMAN METALLOENZYME

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<151> 1999-05-13

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<151> 1999-08-27

<150> 09/563,516

<151> 2000-05-03

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<170> FastSEQ for Windows Version 3.0

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<213> Homo sapiens

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cag	gcc	aag	aca	ttt	ttg	gac	aag	ttt	aac	cac	gaa	gcc	gaa	gac	ctg	151
Gln	Ala	Lys	Thr	Phe	Leu	Asp	Lys	Phe	Asn	His	Glu	Ala	Glu	Asp	Leu	
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ttc	tat	caa	agt	tca	ctt	gct	tct	tgg	aat	tat	aac	acc	aat	att	act	199
Phe	Tyr	Gln	Ser	Ser	Leu	Ala	Ser	Trp	Asn	Tyr	Asn	Thr	Asn	Ile	Thr	
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Glu	Glu	Asn	Val	Gln	Asn	Met	Asn	Asn	Ala	Gly	Asp	Lys	Trp	Ser	Ala	
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ttt	tta	aag	gaa	cag	tcc	aca	ctt	gcc	caa	atg	tat	cca	cta	caa	gaa	295
Phe	Leu	Lys	Glu	Gln	Ser	Thr	Leu	Ala	Gln	Met	Tyr	Pro	Leu	Gln	Glu	
		75						80				85				
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Ile	Gln	Asn	Leu	Thr	Val	Lys	Leu	Gln	Leu	Gln	Ala	Leu	Gln	Gln	Asn	
		90						95				100				
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Gly	Ser	Ser	Val	Leu	Ser	Glu	Asp	Lys	Ser	Lys	Arg	Leu	Asn	Thr	Ile	
105						110				115						
cta	aat	aca	atg	agc	acc	atc	tac	agt	act	gga	aaa	gtt	tgt	aac	cca	439
Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser	Thr	Gly	Lys	Val	Cys	Asn	Pro	
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gat	aat	cca	caa	gaa	tgc	tta	tta	ctt	gaa	cca	ggt	ttg	aat	gaa	ata	487
Asp	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu	Glu	Pro	Gly	Leu	Asn	Glu	Ile	
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Met	Ala	Asn	Ser	Leu	Asp	Tyr	Asn	Glu	Arg	Leu	Trp	Ala	Trp	Glu	Ser	
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Trp	Arg	Ser	Glu	Val	Gly	Lys	Gln	Leu	Arg	Pro	Leu	Tyr	Glu	Glu	Tyr	
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gtg	gtc	ttg	aaa	aat	gag	atg	gca	aga	gca	aat	cat	tat	gag	gac	tat	631
Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg	Ala	Asn	His	Tyr	Glu	Asp	Tyr	
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gac Asp	tac Tyr	agc Ser	cgc Arg	ggc Gly 220	cag Gln	ttg Leu	att Ile	gaa Glu	gat Asp	gtg Val 225	gaa Glu	cat His	acc Thr	ttt Phe	gaa Glu 230	727
gag Glu	att Ile	aaa Lys	cca Pro 235	tta Leu	tat Tyr	gaa Glu	cat His	ctt Leu 240	cat His	gcc Ala	tat Tyr	gtg Val	agg Arg 245	gca Ala	aag Lys	775
ttg Leu	atg Met	aat Asn 250	gcc Ala	tat Tyr	cct Pro	tcc Ser	tat Tyr 255	atc Ile	agt Ser	cca Pro	att Ile	gga Gly 260	tgc Cys	ctc Leu	cct Pro	823
gct Ala 265	cat His	ttg Leu	ctt Leu	ggt Gly	gat Asp	atg Met 270	tgg Trp	ggt Gly	aga Arg	ttt Phe 275	tgg Trp	aca Thr	aat Asn	ctg Leu	tac Tyr	871
tct Ser 280	ttg Leu	aca Thr	gtt Val	ccc Pro	ttt Phe 285	gga Gly	cag Gln	aaa Lys	cca Pro	aac Asn 290	ata Ile	gat Asp	gtt Val	act Thr	gat Asp 295	919
gca Ala	atg Met	gtg Val	gac Asp	cag Gln 300	gcc Ala	tgg Trp	gat Asp	gca Ala	cag Gln 305	aga Arg	ata Ile	ttc Phe	aag Lys	gag Glu 310	gcc Ala	967
gag Glu	aag Lys	ttc Phe	ttt Phe 315	gta Val	tct Ser	gtt Val	ggt Gly	ctt Leu 320	cct Pro	aat Asn	atg Met	act Thr	caa Gln 325	gga Gly	ttc Phe	1015
tgg Trp	gaa Glu	aat Asn 330	tcc Ser	atg Met	cta Leu	acg Thr	gac Asp 335	cca Pro	gga Gly	aat Asn	gtt Val	cag Gln 340	aaa Lys	gca Ala	gtc Val	1063
tgc Cys 345	cat His	ccc Pro	aca Thr	gct Ala	tgg Trp	gac Asp 350	ctg Leu	ggg Gly	aag Lys	ggc Gly	gac Asp 355	ttc Phe	agg Arg	atc Ile	ctt Leu	1111
atg	tgc	aca	aag	gtg	aca	atg	gac	gac	ttc	ctg	aca	gct	cat	cat	gag	1159

Met Cys Thr Lys Val Thr Met Asp Asp Phe Leu Thr Ala His His Glu
 360 365 370 375

atg ggg cat atc cag tat gat atg gca tat gct gca caa cct ttt ctg 1207
 Met Gly His Ile Gln Tyr Asp Met Ala Tyr Ala Ala Gln Pro Phe Leu
 380 385 390

cta aga aat gga gct aat gaa gga ttc cat gaa gct gtt ggg gaa atc 1255
 Leu Arg Asn Gly Ala Asn Glu Gly Phe His Glu Ala Val Gly Glu Ile
 395 400 405

atg tca ctt tct gca gcc aca cct aag cat tta aaa tcc att ggt ctt 1303
 Met Ser Leu Ser Ala Ala Thr Pro Lys His Leu Lys Ser Ile Gly Leu
 410 415 420

ctg tca ccc gat ttt caa gaa gac aat gaa aca gaa ata aac ttc ctg 1351
 Leu Ser Pro Asp Phe Gln Glu Asp Asn Glu Thr Glu Ile Asn Phe Leu
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ctc aaa caa gca ctc acg att gtt ggg act ctg cca ttt act tac atg 1399
 Leu Lys Gln Ala Leu Thr Ile Val Gly Thr Leu Pro Phe Thr Tyr Met
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 Leu Glu Lys Trp Arg Trp Met Val Phe Lys Gly Glu Ile Pro Lys Asp
 460 465 470

cag tgg atg aaa aag tgg tgg gag atg aag cga gag ata gtt ggg gtg 1495
 Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile Val Gly Val
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 Val Glu Pro Val Pro His Asp Glu Thr Tyr Cys Asp Pro Ala Ser Leu
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 Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr Thr Arg Thr
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ctt tac caa ttc cag ttt caa gaa gca ctt tgt caa gca gct aaa cat 1639
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099335-10104

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Pro Arg Thr Glu Val Glu Lys Ala Ile Arg Met Ser Arg Ser Arg Ile
700 705 710

aat gat gct ttc cgt ctg aat gac aac agc cta gag ttt ctg ggg ata 2215
Asn Asp Ala Phe Arg Leu Asn Asp Asn Ser Leu Glu Phe Leu Gly Ile
715 720 725

cag cca aca ctt gga cct cct aac cag ccc cct gtt tcc ata tgg ctg 2263
Gln Pro Thr Leu Gly Pro Pro Asn Gln Pro Pro Val Ser Ile Trp Leu
730 735 740

att gtt ttt gga gtt gtg atg gga gtg ata gtg gtt ggc att gtc atc 2311
Ile Val Phe Gly Val Val Met Gly Val Ile Val Val Gly Ile Val Ile
745 750 755

ctg atc ttc act ggg atc aga gat cgg aag aag aaa aat aaa gca aga 2359
Leu Ile Phe Thr Gly Ile Arg Asp Arg Lys Lys Lys Asn Lys Ala Arg
760 765 770 775

agt gga gaa aat cct tat gcc tcc atc gat att agc aaa gga gaa aat 2407
Ser Gly Glu Asn Pro Tyr Ala Ser Ile Asp Ile Ser Lys Gly Glu Asn
780 785 790

aat cca gga ttc caa aac act gat gat gtt cag acc tcc ttt 2449
Asn Pro Gly Phe Gln Asn Thr Asp Asp Val Gln Thr Ser Phe
795 800 805

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099335.1010

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 <212> PRT
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			20					25					30		
Asn	His	Glu	Ala	Glu	Asp	Leu	Phe	Tyr	Gln	Ser	Ser	Leu	Ala	Ser	Trp
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Asn	Tyr	Asn	Thr	Asn	Ile	Thr	Glu	Glu	Asn	Val	Gln	Asn	Met	Asn	Asn
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Ala	Gly	Asp	Lys	Trp	Ser	Ala	Phe	Leu	Lys	Glu	Gln	Ser	Thr	Leu	Ala
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Gln	Met	Tyr	Pro	Leu	Gln	Glu	Ile	Gln	Asn	Leu	Thr	Val	Lys	Leu	Gln
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Leu	Gln	Ala	Leu	Gln	Gln	Asn	Gly	Ser	Ser	Val	Leu	Ser	Glu	Asp	Lys
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Ser	Lys	Arg	Leu	Asn	Thr	Ile	Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser
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Thr	Gly	Lys	Val	Cys	Asn	Pro	Asp	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu
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Glu	Pro	Gly	Leu	Asn	Glu	Ile	Met	Ala	Asn	Ser	Leu	Asp	Tyr	Asn	Glu
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Arg	Leu	Trp	Ala	Trp	Glu	Ser	Trp	Arg	Ser	Glu	Val	Gly	Lys	Gln	Leu
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Ala	Asn	His	Tyr	Glu	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu
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His	Ala	Tyr	Val	Arg	Ala	Lys	Leu	Met	Asn	Ala	Tyr	Pro	Ser	Tyr	Ile
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Arg	Phe	Trp	Thr	Asn	Leu	Tyr	Ser	Leu	Thr	Val	Pro	Phe	Gly	Gln	Lys
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 Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
 305 310 315 320
 Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro
 325 330 335
 Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly
 340 345 350
 Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp
 355 360 365
 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
 370 375 380
 Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
 385 390 395 400
 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
 405 410 415
 His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn
 420 425 430
 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
 435 440 445
 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe
 450 455 460
 Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met
 465 470 475 480
 Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr
 485 490 495
 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
 500 505 510
 Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala
 515 520 525
 Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile
 530 535 540
 Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu
 545 550 555 560
 Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala
 565 570 575
 Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe
 580 585 590
 Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr
 595 600 605
 Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu
 610 615 620

09707 582650
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Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met
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 Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu
 645 650 655
 Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val
 660 665 670
 Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro
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 Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile
 690 695 700
 Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn
 705 710 715 720
 Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln
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 Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val
 740 745 750
 Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg
 755 760 765
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 805

<210> 3
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 <212> DNA
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 <223> This degenerate sequence encodes the amino acid
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 <223> n = A,T,C or G

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taycarwsnw snytngcnws ntggaaytay aayacnaaya thacngarga raaygtncar	180
aayatgaaya aygcnggnga yaartggwsn gcnttyytna argarcarsw nacnytngcn	240

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aayacnatgw	snacnathta	ywsnacnggn	aargtntgya	ayccngayaa	yccncargar	420
tgyytntytny	tngarccngg	nytnaaygar	athatggcna	aywsnytnga	ytayaaygar	480
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caygcntayg	tnmgngcnaa	rytnatgaay	gcntayccnw	sntayathws	nccnathggg	780
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gcntgggayg	cncarmgnat	httyaargar	gcngaraart	tyttygtnws	ngtnggnytn	960
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caratgathy	tnnttyggnga	rgargaygt	mgngtngcna	ayytnaarcc	nmgnathwsn	2040
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<210> 5

<211> 2638

<212> DNA

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 Met Ser Ser Ser
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tcc tgg ctc ctt ctc agc ctt gtt gct gtt act act gct cag tcc ctc 165
 Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Thr Ala Gln Ser Leu
 5 10 15 20

acc gag gaa aat gcc aag aca ttt tta aac aac ttt aat cag gaa gct 213
 Thr Glu Glu Asn Ala Lys Thr Phe Leu Asn Asn Phe Asn Gln Glu Ala
 25 30 35

gaa gac ctg tct tat caa agt tca ctt gct tct tgg aat tat aat act 261
 Glu Asp Leu Ser Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr
 40 45 50

aac att act gaa gaa aat gcc caa aag atg agt gag gct gca gcc aaa 309
 Asn Ile Thr Glu Glu Asn Ala Gln Lys Met Ser Glu Ala Ala Ala Lys
 55 60 65

tgg tct gcc ttt tat gaa gaa cag tct aag act gcc caa agt ttc tca 357
 Trp Ser Ala Phe Tyr Glu Glu Gln Ser Lys Thr Ala Gln Ser Phe Ser
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cta caa gaa atc cag act ccg atc atc aag cgt caa cta cag gcc ctt 405

0970385-101601

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cag	caa	agt	ggg	tct	tca	gca	ctc	tca	gca	gac	aag	aac	aaa	cag	ttg		453
Gln	Gln	Ser	Gly	Ser	Ser	Ala	Leu	Ser	Ala	Asp	Lys	Asn	Lys	Gln	Leu		
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aac	aca	att	ctg	aac	acc	atg	agc	acc	att	tac	agt	act	gga	aaa	ggt		501
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Cys	Asn	Pro	Lys	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu	Glu	Pro	Gly	Leu		
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Asp	Glu	Ile	Met	Ala	Thr	Ser	Thr	Asp	Tyr	Asn	Ser	Arg	Leu	Trp	Ala		
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Trp	Glu	Gly	Trp	Arg	Ala	Glu	Val	Gly	Lys	Gln	Leu	Arg	Pro	Leu	Tyr		
165					170					175					180		
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Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg	Ala	Asn	Asn	Tyr		
			185						190					195			
aac	gac	tat	ggg	gat	tat	tgg	aga	ggg	gac	tat	gaa	gca	gag	gga	gca		741
Asn	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu	Ala	Glu	Gly	Ala		
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Asp	Gly	Tyr	Asn	Tyr	Asn	Arg	Asn	Gln	Leu	Ile	Glu	Asp	Val	Glu	Arg		
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acc	ttc	gca	gag	atc	aag	cca	ttg	tat	gag	cat	ctt	cat	gcc	tat	gtg		837
Thr	Phe	Ala	Glu	Ile	Lys	Pro	Leu	Tyr	Glu	His	Leu	His	Ala	Tyr	Val		
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agg	agg	aag	ttg	atg	gat	acc	tac	cct	tcc	tac	atc	agc	ccc	act	gga		885
Arg	Arg	Lys	Leu	Met	Asp	Thr	Tyr	Pro	Ser	Tyr	Ile	Ser	Pro	Thr	Gly		
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Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly Arg Phe Trp Thr	
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Asn Leu Tyr Pro Leu Thr Val Pro Phe Ala Gln Lys Pro Asn Ile Asp	
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Val Thr Asp Ala Met Met Asn Gln Gly Trp Asp Ala Glu Arg Ile Phe	
295 300 305	
caa gag gca gag aaa ttc ttt gtt tct gtt ggc ctt cct cat atg act	1077
Gln Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu Pro His Met Thr	
310 315 320	
caa gga ttc tgg gca aac tct atg ctg act gag cca gca gat ggc cgg	1125
Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro Ala Asp Gly Arg	
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aaa gtt gtc tgc cac ccc aca gct tgg gat ctg gga cac gga gac ttc	1173
Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly His Gly Asp Phe	
345 350 355	
aga atc aag atg tgt aca aag gtc aca atg gac aac ttc ttg aca gcc	1221
Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn Phe Leu Thr Ala	
360 365 370	
cat cac gag atg gga cac atc caa tat gac atg gca tat gcc agg caa	1269
His His Glu Met Gly His Ile Gln Tyr Asp Met Ala Tyr Ala Arg Gln	
375 380 385	
cct ttc ctg cta aga aac gga gcc aat gaa ggg ttc cat gaa gct gtt	1317
Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe His Glu Ala Val	
390 395 400	
gga gaa atc atg tca ctt tct gca gct acc ccc aag cat ctg aaa tcc	1365
Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys His Leu Lys Ser	
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att ggt ctt ctg cca tcc gat ttt caa gaa gat agc gaa aca gag ata	1413
Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser Glu Thr Glu Ile	
425 430 435	

aac ttc cta ctg aaa cag gca ttg aca att gtt gga aca cta ccg ttt 1461
 Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly Thr Leu Pro Phe
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act tac atg tta gag aag tgg agg tgg atg gtc ttt cgg ggt gaa att 1509
 Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe Arg Gly Glu Ile
 455 460 465

ccc aaa gag cag tgg atg aaa aag tgg tgg gag atg aag cgg gag atc 1557
 Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile
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gtt ggt gtg gtg gag cct ctg cct cat gat gaa aca tac tgt gac cct 1605
 Val Gly Val Val Glu Pro Leu Pro His Asp Glu Thr Tyr Cys Asp Pro
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gca tct ctg ttc cat gtt tct aat gat tac tca ttc att cga tat tac 1653
 Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr
 505 510 515

aca agg acc att tac caa ttc cag ttt caa gaa gct ctt tgt caa gca 1701
 Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala
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gct aag tat aat ggt tct ctg cac aaa tgt gac atc tca aat tcc act 1749
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 550 555 560

ccc tgg acc aaa gcc ttg gaa aat gtg gta gga gca agg aat atg gat 1845
 Pro Trp Thr Lys Ala Leu Glu Asn Val Val Gly Ala Arg Asn Met Asp
 565 570 575 580

gta aaa cca ctg ctc aat tac ttc caa ccg ttg ttt gac tgg ctg aaa 1893
 Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe Asp Trp Leu Lys
 585 590 595

gag cag aac aga aat tct ttt gtg ggg tgg aac act gaa tgg agc cca 1941

09978385-10464

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tat gcc gac caa agc att aaa gtg agg ata agc cta aaa tca gct ctt	1989
Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu Lys Ser Ala Leu	
615 620 625	
gga gct aat gca tat gaa tgg acc aac aac gaa atg ttc ctg ttc cga	2037
Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met Phe Leu Phe Arg	
630 635 640	
tca tct gtt gca tat gcc atg aga aag tat ttt tca ata atc aaa aac	2085
Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Phe Ser Ile Ile Lys Asn	
645 650 655 660	
cag aca gtt cct ttt cta gag gaa gat gta cga gtg agc gat ttg aaa	2133
Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val Ser Asp Leu Lys	
665 670 675	
cca aga gtc tcc ttc tac ttc ttt gtc acc tca ccc caa aat gtg tct	2181
Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro Gln Asn Val Ser	
680 685 690	
gat gtc att cct aga agt gaa gtt gaa gat gcc atc agg atg tct cgg	2229
Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile Arg Met Ser Arg	
695 700 705	
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Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn Ser Leu Glu Phe	
710 715 720	
ctg ggg att cac cca aca ctt gag cca cct tac cag cct cct gtc acc	2325
Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln Pro Pro Val Thr	
725 730 735 740	
ata tgg ctg att att ttt ggt gtt gtg atg gca ctg gta gtg gtt ggc	2373
Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu Val Val Val Gly	
745 750 755	
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0970305-10101

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 Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met Asp Ile Gly Lys
 775 780 785

gga gaa agc aat gca gga ttc caa aac agt gat gat gct cag act tcc 2517
 Gly Glu Ser Asn Ala Gly Phe Gln Asn Ser Asp Asp Ala Gln Thr Ser
 790 795 800

ttt tagcaaagca cttgtcatct tcctgtatgt aaatgctaac ttcatagtac 2570
 Phe
 805

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<400> 6

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 Asn Gln Glu Ala Glu Asp Leu Ser Tyr Gln Ser Ser Leu Ala Ser Trp
 35 40 45
 Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Ala Gln Lys Met Ser Glu
 50 55 60
 Ala Ala Ala Lys Trp Ser Ala Phe Tyr Glu Glu Gln Ser Lys Thr Ala
 65 70 75 80
 Gln Ser Phe Ser Leu Gln Glu Ile Gln Thr Pro Ile Ile Lys Arg Gln
 85 90 95
 Leu Gln Ala Leu Gln Gln Ser Gly Ser Ser Ala Leu Ser Ala Asp Lys
 100 105 110
 Asn Lys Gln Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser
 115 120 125

09703E-101E4

Thr Gly Lys Val Cys Asn Pro Lys Asn Pro Gln Glu Cys Leu Leu Leu
 130 135 140
 Glu Pro Gly Leu Asp Glu Ile Met Ala Thr Ser Thr Asp Tyr Asn Ser
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 Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg
 180 185 190
 Ala Asn Asn Tyr Asn Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu
 195 200 205
 Ala Glu Gly Ala Asp Gly Tyr Asn Tyr Asn Arg Asn Gln Leu Ile Glu
 210 215 220
 Asp Val Glu Arg Thr Phe Ala Glu Ile Lys Pro Leu Tyr Glu His Leu
 225 230 235 240
 His Ala Tyr Val Arg Arg Lys Leu Met Asp Thr Tyr Pro Ser Tyr Ile
 245 250 255
 Ser Pro Thr Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly
 260 265 270
 Arg Phe Trp Thr Asn Leu Tyr Pro Leu Thr Val Pro Phe Ala Gln Lys
 275 280 285
 Pro Asn Ile Asp Val Thr Asp Ala Met Met Asn Gln Gly Trp Asp Ala
 290 295 300
 Glu Arg Ile Phe Gln Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
 305 310 315 320
 Pro His Met Thr Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro
 325 330 335
 Ala Asp Gly Arg Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly
 340 345 350
 His Gly Asp Phe Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn
 355 360 365
 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
 370 375 380
 Tyr Ala Arg Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
 385 390 395 400
 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
 405 410 415
 His Leu Lys Ser Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser
 420 425 430
 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
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 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe
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09973385.101501

Arg Gly Glu Ile Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met
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 Lys Arg Glu Ile Val Gly Val Val Glu Pro Leu Pro His Asp Glu Thr
 485 490 495
 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
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 Ile Arg Tyr Tyr Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala
 515 520 525
 Leu Cys Gln Ala Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile
 530 535 540
 Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu
 545 550 555 560
 Gly Asn Ser Glu Pro Trp Thr Lys Ala Leu Glu Asn Val Val Gly Ala
 565 570 575
 Arg Asn Met Asp Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe
 580 585 590
 Asp Trp Leu Lys Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr
 595 600 605
 Glu Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu
 610 615 620
 Lys Ser Ala Leu Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met
 625 630 635 640
 Phe Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Phe Ser
 645 650 655
 Ile Ile Lys Asn Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val
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 Ser Asp Leu Lys Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro
 675 680 685
 Gln Asn Val Ser Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile
 690 695 700
 Arg Met Ser Arg Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn
 705 710 715 720
 Ser Leu Glu Phe Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln
 725 730 735
 Pro Pro Val Thr Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu
 740 745 750
 Val Val Val Gly Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg
 755 760 765
 Lys Lys Lys Asn Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met
 770 775 780
 Asp Ile Gly Lys Gly Glu Ser Asn Ala Gly Phe Gln Asn Ser Asp Asp
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09970305-101604

Ala Gln Thr Ser Phe
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<210> 7

<211> 2415

<212> DNA

<213> Artificial Sequence

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<223> This degenerate sequence encodes the amino acid
sequence of SEQ ID NO:6.

<221> misc_feature

<222> (1)...(2415)

<223> n = A,T,C or G

<400> 7

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taycarwsnw	snytnecnws	ntggaaytay	aayacnaaya	thacngarga	raaygcncar	180
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carwsnttyw	snytnrcarga	rathcaracn	ccnathatha	armgncaryt	ncargcnytn	300
carcarwsng	gnwsnwsngc	nytnwsngcn	gayaaraaya	arcarytnaa	yacnathytn	360
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gargartayg	tngtnytnaa	raaygaratg	gcnmngncna	ayaaytayaa	ygaytayggg	600
gaytaytggm	gnngngayta	ygargcngar	ggngcngayg	gntayaayta	yaaymgnaay	660
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caygargcng	tngngarat	hatgwsnytn	wsngcngcna	cncncaarca	yytnaarwsn	1260
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09974335.10661

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 caracngtnc cnttyytnga rgargaygtm mngtnwsng ayytnaarcc nmngtnwsn 2040
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<211> 2638

<212> DNA

<213> Mouse

<220>

<221> CDS

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 Met Ser Ser Ser
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tcc tgg ctc ctt ctc agc ctt gtt gct gtt act act gct cag tcc ctc 165
 Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Thr Ala Gln Ser Leu
 5 10 15 20

acc gag gaa aat gcc aag aca ttt tta aac aac ttt aat cag gag gct 213
 Thr Glu Glu Asn Ala Lys Thr Phe Leu Asn Asn Phe Asn Gln Glu Ala
 25 30 35

gaa gac ctg tct tat caa agt tca ctt gct tct tgg aat tat aat act 261
 Glu Asp Leu Ser Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr
 40 45 50

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Trp	Ser	Ala	Phe	Tyr	Glu	Glu	Gln	Ser	Lys	Thr	Ala	Gln	Ser	Phe	Ser	
		70					75				80					
cta	caa	gaa	atc	cag	act	ccg	atc	atc	aag	cgt	caa	cta	cag	gcc	ctt	405
Leu	Gln	Glu	Ile	Gln	Thr	Pro	Ile	Ile	Lys	Arg	Gln	Leu	Gln	Ala	Leu	
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Gln	Gln	Ser	Gly	Ser	Ser	Ala	Leu	Ser	Ala	Asp	Lys	Asn	Lys	Gln	Leu	
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Cys	Asn	Pro	Arg	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu	Glu	Pro	Gly	Leu	
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Asp	Glu	Ile	Met	Ala	Thr	Ser	Thr	Asp	Tyr	Asn	Ser	Arg	Leu	Trp	Ala	
		150				155					160					
tgg	gag	ggc	tgg	agg	gct	gag	gtt	ggc	aag	cag	ctg	agg	ccg	ttg	tat	645
Trp	Glu	Gly	Trp	Arg	Ala	Glu	Val	Gly	Lys	Gln	Leu	Arg	Pro	Leu	Tyr	
		165				170				175					180	
gaa	gag	tat	gtg	gtc	ctg	aaa	aac	gag	atg	gca	aga	gca	aac	aat	tat	693
Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg	Ala	Asn	Asn	Tyr	
				185					190					195		
aac	gac	tat	ggg	gat	tat	tgg	aga	ggg	gac	tat	gaa	gca	gag	gga	gca	741
Asn	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu	Ala	Glu	Gly	Ala	
			200					205				210				
gat	ggc	tac	aac	tat	aac	cgt	aac	cag	ttg	att	gaa	gat	gta	gaa	cgt	789

Asp Gly Tyr Asn Tyr Asn Arg Asn Gln Leu Ile Glu Asp Val Glu Arg	
215 220 225	
acc ttc gca gag atc aag cca ttg tat gag cat ctt cat gcc tat gtg	837
Thr Phe Ala Glu Ile Lys Pro Leu Tyr Glu His Leu His Ala Tyr Val	
230 235 240	
agg agg aag ttg atg gat acc tac cct tcc tac atc agc ccc act gga	885
Arg Arg Lys Leu Met Asp Thr Tyr Pro Ser Tyr Ile Ser Pro Thr Gly	
245 250 255 260	
tgc ctc cct gcc cat ttg ctt ggt gat atg tgg ggt aga ttt tgg aca	933
Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly Arg Phe Trp Thr	
265 270 275	
aat ctg tac cct ttg act gtt ccc ttt gca cag aaa cca aac ata gat	981
Asn Leu Tyr Pro Leu Thr Val Pro Phe Ala Gln Lys Pro Asn Ile Asp	
280 285 290	
gtt act gat gca atg atg aat cag ggc tgg gat gca gaa agg ata ttt	1029
Val Thr Asp Ala Met Met Asn Gln Gly Trp Asp Ala Glu Arg Ile Phe	
295 300 305	
caa gag gca gag aaa ttc ttt gtt tct gtt ggc ctt cct cat atg act	1077
Gln Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu Pro His Met Thr	
310 315 320	
caa gga ttc tgg gca aac tct atg ctg act gag cca gca gat ggc cgg	1125
Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro Ala Asp Gly Arg	
325 330 335 340	
aaa gtt gtc tgc cac ccc aca gct tgg gat ctg gga cac gga gac ttc	1173
Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly His Gly Asp Phe	
345 350 355	
aga atc aag atg tgt aca aag gtc aca atg gac aac ttc ttg aca gcc	1221
Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn Phe Leu Thr Ala	
360 365 370	
cat cac gag atg gga cac atc caa tat gac atg gca tat gcc agg caa	1269

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His	His	Glu	Met	Gly	His	Ile	Gln	Tyr	Asp	Met	Ala	Tyr	Ala	Arg	Gln	
		375					380									
cct	ttc	ctg	cta	aga	aac	gga	gcc	aat	gaa	ggg	ttc	cat	gaa	gct	gtt	1317
Pro	Phe	Leu	Leu	Arg	Asn	Gly	Ala	Asn	Glu	Gly	Phe	His	Glu	Ala	Val	
	390					395					400					
gga	gaa	atc	atg	tca	ctt	tct	gca	gct	acc	ccc	aag	cat	ctg	aaa	tcc	1365
Gly	Glu	Ile	Met	Ser	Leu	Ser	Ala	Ala	Thr	Pro	Lys	His	Leu	Lys	Ser	
405					410					415					420	
att	ggt	ctt	ctg	cca	tcc	gat	ttt	caa	gaa	gat	agc	gaa	aca	gag	ata	1413
Ile	Gly	Leu	Leu	Pro	Ser	Asp	Phe	Gln	Glu	Asp	Ser	Glu	Thr	Glu	Ile	
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aac	ttc	cta	ctg	aaa	cag	gca	ttg	aca	att	gtt	gga	aca	cta	ccg	ttt	1461
Asn	Phe	Leu	Leu	Lys	Gln	Ala	Leu	Thr	Ile	Val	Gly	Thr	Leu	Pro	Phe	
		440						445					450			
act	tac	atg	tta	gag	aag	tgg	agg	tgg	atg	gtc	ttt	cgg	ggt	gaa	att	1509
Thr	Tyr	Met	Leu	Glu	Lys	Trp	Arg	Trp	Met	Val	Phe	Arg	Gly	Glu	Ile	
		455					460					465				
ccc	aaa	gag	cag	tgg	atg	aaa	aag	tgg	tgg	gag	atg	aag	cgg	gag	atc	1557
Pro	Lys	Glu	Gln	Trp	Met	Lys	Lys	Trp	Trp	Glu	Met	Lys	Arg	Glu	Ile	
	470					475					480					
gtt	ggt	gtg	gtg	gag	cct	ctg	cct	cgt	gat	gaa	aca	tac	tgt	gac	cct	1605
Val	Gly	Val	Val	Glu	Pro	Leu	Pro	Arg	Asp	Glu	Thr	Tyr	Cys	Asp	Pro	
485					490					495					500	
gca	tct	ctg	ttc	cat	gtt	tct	aat	gat	tac	tca	ttc	att	cga	tat	tac	1653
Ala	Ser	Leu	Phe	His	Val	Ser	Asn	Asp	Tyr	Ser	Phe	Ile	Arg	Tyr	Tyr	
				505					510					515		
aca	agg	acc	att	tac	caa	ttc	cag	ttt	caa	gaa	gct	ctt	tgt	caa	gca	1701
Thr	Arg	Thr	Ile	Tyr	Gln	Phe	Gln	Phe	Gln	Glu	Ala	Leu	Cys	Gln	Ala	
				520				525					530			
gct	aag	tat	aat	ggt	tct	ctg	cac	aaa	tgt	gac	atc	tca	aat	tcc	act	1749

Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile Ser Asn Ser Thr	
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gaa gct ggg cag aag ttg ctc aag atg ctg agt ctt gga aat tca gag	1797
Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu Gly Asn Ser Glu	
550 555 560	
ccc tgg acc gaa gcc ttg gaa aat gtg gta gga gca agg aat atg gat	1845
Pro Trp Thr Glu Ala Leu Glu Asn Val Val Gly Ala Arg Asn Met Asp	
565 570 575 580	
gta aaa cca ctg ctc aat tac ttc caa ccg ttg ttt gac tgg ctg aaa	1893
Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe Asp Trp Leu Lys	
585 590 595	
gag cag aac aga aat tct ttt gtg ggg tgg aac act gaa tgg agc cca	1941
Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr Glu Trp Ser Pro	
600 605 610	
tat gcc gac caa agc att aaa gtg agg ata agc cta aaa tca gct ctt	1989
Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu Lys Ser Ala Leu	
615 620 625	
gga gct aat gca tat gaa tgg acc aac aac gaa atg ttc ctg ttc cga	2037
Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met Phe Leu Phe Arg	
630 635 640	
tca tct gtt gca tat gcc atg aga aag tat tct tca ata atc aaa aac	2085
Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Ser Ser Ile Ile Lys Asn	
645 650 655 660	
cag aca gtt cct ttt cta gag gaa gat gta cga gtg agt gat ttg aaa	2133
Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val Ser Asp Leu Lys	
665 670 675	
cca aga gtc tcc ttc tac ttc ttt gtc acc tca ccc caa aat gtg tct	2181
Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro Gln Asn Val Ser	
680 685 690	
gat gtc att cct aga agt gaa gtt gaa gat gcc atc agg atg tct cgg	2229

Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile Arg Met Ser Arg
 695 700 705

ggc cgc atc aat gat gtc ttt ggc ctg aat gat aac agc ctg gag ttt 2277
 Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn Ser Leu Glu Phe
 710 715 720

ctg ggg att cac cca aca ctt gag cca cct tac cag cct cct gtc acc 2325
 Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln Pro Pro Val Thr
 725 730 735 740

ata tgg ctg att att ttt ggt gtt gtg atg gca ctg gta gtg gtt ggc 2373
 Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu Val Val Val Gly
 745 750 755

atc atc atc ctg att gtc act ggg atc aaa ggt cga aag aag aaa aat 2421
 Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg Lys Lys Lys Asn
 760 765 770

gaa aca aaa aga gaa gag aac cct tat gac tcg atg gac att gga aaa 2469
 Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met Asp Ile Gly Lys
 775 780 785

gga gaa agc aat gca gga ttc caa aac agt gat gat gct cag act tcc 2517
 Gly Glu Ser Asn Ala Gly Phe Gln Asn Ser Asp Asp Ala Gln Thr Ser
 790 795 800

ttt tagcaaagca cttgtcatct tcctgtatgt aaatgctaac ttcatagtac 2570
 Phe
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			20					25					30		
Asn	Gln	Glu	Ala	Glu	Asp	Leu	Ser	Tyr	Gln	Ser	Ser	Leu	Ala	Ser	Trp
		35				40						45			
Asn	Tyr	Asn	Thr	Asn	Ile	Thr	Glu	Glu	Asn	Ala	Gln	Lys	Met	Ser	Glu
	50				55						60				
Ala	Ala	Ala	Lys	Trp	Ser	Ala	Phe	Tyr	Glu	Glu	Gln	Ser	Lys	Thr	Ala
65				70					75					80	
Gln	Ser	Phe	Ser	Leu	Gln	Glu	Ile	Gln	Thr	Pro	Ile	Ile	Lys	Arg	Gln
			85					90						95	
Leu	Gln	Ala	Leu	Gln	Gln	Ser	Gly	Ser	Ser	Ala	Leu	Ser	Ala	Asp	Lys
		100					105						110		
Asn	Lys	Gln	Leu	Asn	Thr	Ile	Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser
	115				120							125			
Thr	Gly	Lys	Val	Cys	Asn	Pro	Arg	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu
	130				135						140				
Glu	Pro	Gly	Leu	Asp	Glu	Ile	Met	Ala	Thr	Ser	Thr	Asp	Tyr	Asn	Ser
145				150						155				160	
Arg	Leu	Trp	Ala	Trp	Glu	Gly	Trp	Arg	Ala	Glu	Val	Gly	Lys	Gln	Leu
			165					170						175	
Arg	Pro	Leu	Tyr	Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg
		180					185					190			
Ala	Asn	Asn	Tyr	Asn	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu
	195				200						205				
Ala	Glu	Gly	Ala	Asp	Gly	Tyr	Asn	Tyr	Asn	Arg	Asn	Gln	Leu	Ile	Glu
210				215						220					
Asp	Val	Glu	Arg	Thr	Phe	Ala	Glu	Ile	Lys	Pro	Leu	Tyr	Glu	His	Leu
225				230					235					240	
His	Ala	Tyr	Val	Arg	Arg	Lys	Leu	Met	Asp	Thr	Tyr	Pro	Ser	Tyr	Ile
			245				250							255	
Ser	Pro	Thr	Gly	Cys	Leu	Pro	Ala	His	Leu	Leu	Gly	Asp	Met	Trp	Gly
		260				265						270			
Arg	Phe	Trp	Thr	Asn	Leu	Tyr	Pro	Leu	Thr	Val	Pro	Phe	Ala	Gln	Lys
	275				280						285				
Pro	Asn	Ile	Asp	Val	Thr	Asp	Ala	Met	Met	Asn	Gln	Gly	Trp	Asp	Ala
	290				295						300				
Glu	Arg	Ile	Phe	Gln	Glu	Ala	Glu	Lys	Phe	Phe	Val	Ser	Val	Gly	Leu
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Pro His Met Thr Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro
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 Ala Asp Gly Arg Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly
 340 345 350
 His Gly Asp Phe Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn
 355 360 365
 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
 370 375 380
 Tyr Ala Arg Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
 385 390 395 400
 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
 405 410 415
 His Leu Lys Ser Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser
 420 425 430
 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
 435 440 445
 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe
 450 455 460
 Arg Gly Glu Ile Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met
 465 470 475 480
 Lys Arg Glu Ile Val Gly Val Val Glu Pro Leu Pro Arg Asp Glu Thr
 485 490 495
 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
 500 505 510
 Ile Arg Tyr Tyr Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala
 515 520 525
 Leu Cys Gln Ala Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile
 530 535 540
 Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu
 545 550 555 560
 Gly Asn Ser Glu Pro Trp Thr Glu Ala Leu Glu Asn Val Val Gly Ala
 565 570 575
 Arg Asn Met Asp Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe
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 Asp Trp Leu Lys Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr
 595 600 605
 Glu Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu
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 Lys Ser Ala Leu Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met
 625 630 635 640
 Phe Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Ser Ser
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09973385.101641

Ile Ile Lys Asn Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val
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 Ser Asp Leu Lys Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro
 675 680 685
 Gln Asn Val Ser Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile
 690 695 700
 Arg Met Ser Arg Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn
 705 710 715 720
 Ser Leu Glu Phe Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln
 725 730 735
 Pro Pro Val Thr Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu
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 Val Val Val Gly Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg
 755 760 765
 Lys Lys Lys Asn Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met
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